This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims: Please **amend** the claims as follows:

We claim:

Claims 1.–70. (Cancelled)

Claim 71. (Currently Amended) A method according to claim 74 ~~65~~, wherein determination of the released identifier sequence tract(s) is achieved by mass spectrometry.

Claim 72. (Currently Amended) A method of claim 71, wherein the mass spectrometry is matrix-assisted laser desorption/ionization time-of-flight (MALDI-ToF) spectrometry.

Claim 73. (Cancelled)

Claim 74. (Currently Amended) A method of identifying a recombinant ~~protein~~ antibody or an antigen-binding portion thereof which binds to ~~a target~~ an antigen of interest, said antibody being a member of a library of antibodies, wherein each antibody member comprises within its amino acid sequence or terminal to it, one or more individual identifier sequence amino acid tracts which is unique to said antibody and wherein said sequence is further flanked by one or more protease sensitive sites ~~wherein the protein is a member of the library as defined in claim 52~~, comprising ~~the following steps~~:

(i) ~~bringing each of the individual proteins~~ contacting said antibody of the library with one or more of said antigens to form an antigen-antibody complex ~~comprising said one or more individual identifier sequence tracts and said protease sensitive site(s) in contact or association with one or more of said targets of interest~~,

(ii) isolating the antigen-antibody complex of (i) ~~formed by the individual protein and the target of interest~~,

(iii) digesting said antigen-antibody complex to cleave the ~~introduced~~ protease sensitive sites ~~releasing~~ and release said individual identifier sequence tract(s), and

(iv) determining said released sequence tract(s) and using such sequence information to recover the individual ~~protein library~~ antibody member from the library, and

(v) ~~including one or more further rounds of~~ optionally repeating each of (i) to (iv) iteratively for screening and enrichment for ~~a protein~~ an antibody which binds to the ~~target~~ antigen of interest.

Claim 75. (Currently Amended) ~~A~~ The method of claim 74 ~~64~~, wherein said protease sensitive site is the site for enterokinase, genease, thrombin or Factor Xa digestion.

Claim 76. (Currently Amended) ~~A~~ The method of claim 74 ~~64~~, wherein said protease sensitive site is the site for endoprotease digestion.

Claim 77. (Previously Presented) ~~A~~ The method of claim 74 ~~73~~, wherein the antigen-binding antibody domain is an Fv domain comprising a VH and VL chain.

Claim 78. (Previously Presented) ~~A~~ The method of claim 77, wherein said identifier sequence tract is C-terminal to the Fv domain.

Claim 79. (Cancelled)

Claim 80. (New) The method as claimed in claim 74, wherein the identifier sequence tract is detected by MS/MS analysis.

Claim 81. (New) The method as claimed in claim 71, wherein said determination of the released identifier sequence tract(s) further comprises performing high performance liquid chromatography (HPLC).

Claim 82. (New) The method as claimed in claim 74, wherein the resultant antigen-antibody complex is subjected to physical fractionation and/or chemical tagging as part of the isolation step (ii).

Claim 83. (New) The method as claimed in claim 74, wherein the antibody or an antigen binding portion thereof is bound to a solid phase.

Claim 84. (New) The method as claimed in claim 83, wherein the antibodies are derivatized with biotin prior to binding to a solid phase comprising avidin or streptavidin.

Claim 85. (New) The method as claimed in claim 83, wherein the antibodies are derivatized with a ligand prior to binding to a phase comprising a ligand-specific affinity reagent.

Claim 86. (New) The method as claimed in claim 85, wherein the ligand is dinitrophenol or fluorescein.

Claim 87. (New) The method as claimed in claim 85, wherein the antibody is derivatized at the N-terminus with phenyl isothiocyanate or at the C-terminus via carboximide activation.

Claim 88. (New) The method as claimed in claim 74, wherein the antibody is a monoclonal antibody or an Fab, Fv or a single-chain Fv portion thereof.

Claim 89. (New) The method as claimed in claim 74, wherein the protease recognition site is

Asp-Asp-Asp-Asp-Lys (SEQ ID NO: 1),

Ile-Glu-Gly-Arg (SEQ ID NO: 4),

Pro-Gly-Ala-Ala-His-Tyr (SEQ ID NO: 5), or

Leu-Val-Pro-Arg-Gly-Ser (SEQ ID NO: 6)

Claim 90. (New) The method as claimed in claim 74, wherein the protease recognition site comprises an N-terminal

Asp-Asp-Asp-Asp (SEQ ID NO: 7) for the identification of N terminal Lys,

Pro-Gly-Ala-Ala-His (SEQ ID NO: 8) for the identification of N terminal Tyr,

Leu-Val-Pro-Arg (SEQ ID NO: 9) for the identification of N terminal Gly-Ser; or

Leu-Val-Pro-Arg-Gly (SEQ ID NO: 10) for the identification of N terminal Ser.

Claim 91. (New) A method of identifying a recombinant antibody or an antigen-binding portion thereof which binds to an antigen of interest, said antibody being a member of a

library of antibodies, wherein each antibody member comprises within its amino acid sequence or terminal to it, one or more individual identifier sequence amino acid tracts which is unique to said antibody and wherein said sequence is further flanked by one or more protease sensitive sites, comprising:

(i) contacting said antibody of the library with one or more of said antigens to form an antigen-antibody complex,

(ii) isolating the antigen-antibody complex of (i),

(iii) digesting said antigen-antibody complex to cleave the protease sensitive sites and release said individual identifier sequence tract(s), and

(iv) determining said released sequence tract(s) and using such sequence information to recover the individual antibody member from the library, and

(v) optionally repeating each of (i) to (iv) iteratively for screening and enrichment for an antibody which binds to the antigen of interest,

wherein

said protease sensitive site is the site for enterokinase, genease, thrombin, Factor Xa digestion, or endoprotease digestion,

said antigen-binding antibody domain is an Fv domain comprising a VH and VL chain, and

said identifier sequence tract is C-terminal to the Fv domain.